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P.2.

RAW SEQUENCE LISTING   DATE: 08/24/2000
PATENT APPLICATION: US/09/638,648   TIME: 16:21:24

Input Set : A:\620971.app
Output Set: N:\CRF3\08232000\I638648.raw

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   3 <110> APPLICANT: Stern, David M.
   4         Schmidt, Ann Marie
   5         Yan, Shi Du
   6         Zlokovic, Berislav
   8 <120> TITLE OF INVENTION: A METHOD TO INCREASE CEREBRAL BLOOD FLOW IN AMYLOID
   9         ANGIOPATHY
  11 <130> FILE REFERENCE: 0575/62097
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/638,648
  14 <141> CURRENT FILING DATE: 2000-08-14
  16 <160> NUMBER OF SEQ ID NOS: 6
  18 <170> SOFTWARE: PatentIn Ver. 2.1
  20 <210> SEQ ID NO: 1
  21 <211> LENGTH: 416
  22 <212> TYPE: PRT
  23 <213> ORGANISM: Bos Taurus
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  29 Gly Gly Thr Val Thr Gly Asp Gln Asn Ile Thr Ala Arg Ile Gly Lys
  30                  20                  25                  30
  32 Pro Leu Val Leu Asn Cys Lys Gly Ala Pro Lys Lys Pro Pro Gln Gln
  33          35                  40                  45
  35 Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu
  36          50                  55                  60
  38 Ser Pro Gln Gly Asp Pro Trp Asp Ser Val Ala Arg Val Leu Pro Asn
  39  65               70                  75                  80
  41 Gly Ser Leu Leu Leu Pro Ala Val Gly Ile Gln Asp Glu Gly Thr Phe
  42                  85                  90                  95
  44 Arg Cys Arg Ala Thr Ser Arg Ser Gly Lys Glu Thr Lys Ser Asn Tyr
  45          100                 105                 110
  47 Arg Val Arg Val Tyr Gln Ile Pro Gly Lys Pro Glu Ile Val Asp Pro
  48          115                 120                 125
  50 Ala Ser Glu Leu Met Ala Gly Val Pro Asn Lys Val Gly Thr Cys Val
  51          130                 135                 140
  53 Ser Glu Gly Gly Tyr Pro Ala Gly Thr Leu Asn Trp Leu Leu Asp Gly
  54 145                 150                 155                 160
  56 Lys Thr Leu Ile Pro Asp Gly Lys Gly Val Ser Val Lys Glu Glu Thr
  57              165                 170                 175
  59 Lys Arg His Pro Lys Thr Gly Leu Phe Thr Leu His Ser Glu Leu Met
  60          180                 185                 190
  62 Val Thr Pro Ala Arg Gly Gly Ala Leu His Pro Thr Phe Ser Cys Ser
  63          195                 200                 205
  65 Phe Thr Pro Gly Leu Pro Arg Arg Ala Leu His Thr Ala Pro Ile
  66 210                 215                 220
  68 Gln Leu Arg Val Trp Ser Glu His Arg Gly Gly Glu Gly Pro Asn Val
  69 225                 230                 235                 240
  71 Asp Ala Val Pro Leu Lys Glu Val Gln Leu Val Val Glu Pro Glu Gly
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 74 Gly Ala Val Ala Pro Gly Gly Thr Val Thr Leu Thr Cys Glu Ala Pro
 75             260                265                270
 77 Ala Gln Pro Pro Pro Gln Ile His Trp Ile Lys Asp Gly Arg Pro Leu
 78         275                280                285
 80 Pro Leu Pro Pro Gly Pro Met Leu Leu Leu Pro Glu Val Gly Pro Glu
 81     290                295                300
 83 Asp Gln Gly Thr Tyr Ser Cys Val Ala Thr His Pro Ser His Gly Pro
 84 305                310                315                320
 86 Gln Glu Ser Arg Ala Val Ser Val Thr Ile Ile Glu Thr Gly Glu Glu
 87             325                330                335
 89 Gly Thr Thr Ala Gly Ser Val Glu Gly Pro Gly Leu Glu Thr Leu Ala
 90             340                345                350
 92 Leu Thr Leu Gly Ile Leu Gly Gly Leu Gly Thr Val Ala Leu Leu Ile
 93     355                360                365
 95 Gly Val Ile Val Trp His Arg Arg Arg Gln Arg Lys Gly Gln Glu Arg
 96     370                375                380
 98 Lys Val Pro Glu Asn Gln Glu Glu Glu Glu Glu Glu Arg Ala Glu Leu
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109 <211> LENGTH: 1426
110 <212> TYPE: DNA
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116 tgcaagggag cccccaagaa accaccccag cagctggaat ggaaactgaa cacaggccgg 180
117 acagaagctt ggaaagtcct gtctccccag ggagacccct gggatagcgt ggctcgggtc 240
118 ctccccaacg gctccctcct cctgccggct gttgggatcc aggatgaggg gactttccgg 300
119 tgccgggcaa cgagccggag cggaaaggag accaagtcta actaccgagt ccgagtctat 360
120 cagattcctg ggaagccaga aattgttgat cctgcctctg aactcatggc tggtgtcccc 420
121 aataaggtgg ggacatgtgt gtccgagggg ggctaccctg cagggactct taactggctc 480
122 ttggatggga aaactctgat tcctgatggc aaaggagtgt cagtgaagga agagaccaag 540
123 agacacccaa agacagggct tttcacgctc cattcggagc tgatggtgac cccagctcgg 600
124 ggaggagctc tccaccccac cttctcctgt agcttcaccc ctggccttcc ccggcgccga 660
125 gccctgcaca cggcccccat ccagctcagg gtctggagtg agcaccgagg tggggagggc 720
126 cccaacgtgg acgctgtgcc actgaaggaa gtccagttgg tggtagagcc agaaggggga 780
127 gcagtagctc ctggtggtac tgtgaccttg acctgtgaag cccccgccca gcccccacct 840
128 caaatccact ggatcaagga tggcaggccc ctgccccttc ccctggcc catgctgctc 900
129 ctcccagagg tagggcctga ggaccaggga acctacagtt gtgtggccac ccatcccagc 960
130 catgggcccc aggagagccg tgctgtcagc gtcacgatca tcgaaacagg cgaggagggg 1020
131 acgactgcag gctctgtgga agggccgggg ctggaaaccc tagccctgac cctggggatc 1080
132 ctgggaggcc tggggacagt cgccctgctc attggggtca tcgtgtggca tcgaaggcgg 1140
133 caacgcaaag gacaggagag gaaggtcccg gaaaaccagg aggaggaaga ggaggagaga 1200
134 gcggaactga accagccaga ggagcccgag gcggcagaga gcagcacagg agggccttga 1260
135 ggagcccacg gccagacccg atccatcagc ccctttttctt ttccacact ctgttctggc 1320
136 cccagaccag ttctcctctg tataatctcc agcccacatc tcccaaactt tcttccacaa 1380
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/638,648

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143 <213> ORGANISM: Human
145 <400> SEQUENCE: 3
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149 Trp Gly Ala Val Val Gly Ala Gln Asn Ile Thr Ala Arg Ile Gly Glu
150   20   25   30
152 Pro Leu Val Leu Lys Cys Lys Gly Ala Pro Lys Lys Pro Pro Gln Arg
153   35   40   45
155 Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu
156   50   55   60
158 Ser Pro Gln Gly Gly Gly Pro Trp Asp Ser Val Ala Arg Val Leu Pro
159 65   70   75   80
161 Asn Gly Ser Leu Phe Leu Pro Ala Val Gly Ile Gln Asp Glu Gly Ile
162   85   90   95
164 Phe Arg Cys Arg Ala Met Asn Arg Asn Gly Lys Glu Thr Lys Ser Asn
165   100   105   110
167 Tyr Arg Val Arg Val Tyr Gln Ile Pro Gly Lys Pro Glu Ile Val Asp
168   115   120   125
170 Ser Ala Ser Glu Leu Thr Ala Gly Val Pro Asn Lys Val Gly Thr Cys
171   130   135   140
173 Val Ser Glu Gly Ser Tyr Pro Ala Gly Thr Leu Ser Trp His Leu Asp
174 145   150   155   160
176 Gly Lys Pro Leu Val Pro Asn Glu Lys Gly Val Ser Val Lys Glu Gln
177   165   170   175
179 Thr Arg Arg His Pro Glu Thr Gly Leu Phe Thr Leu Gln Ser Glu Leu
180   180   185   190
182 Met Val Thr Pro Ala Arg Gly Gly Asp Pro Arg Pro Thr Phe Ser Cys
183   195   200   205
185 Ser Phe Ser Pro Gly Leu Pro Arg His Arg Ala Leu Arg Thr Ala Pro
186   210   215   220
188 Ile Gln Pro Arg Val Trp Glu Pro Val Pro Leu Glu Glu Val Gln Leu
189 225   230   235   240
191 Val Val Glu Pro Glu Gly Gly Ala Val Ala Pro Gly Gly Thr Val Thr
192   245   250   255
194 Leu Thr Cys Glu Val Pro Ala Gln Pro Ser Pro Gln Ile His Trp Met
195   260   265   270
197 Lys Asp Gly Val Pro Leu Pro Leu Pro Pro Ser Pro Val Leu Ile Leu
198   275   280   285
200 Pro Glu Ile Gly Pro Gln Asp Gln Gly Thr Tyr Ser Cys Val Ala Thr
201   290   295   300
203 His Ser Ser His Gly Pro Gln Glu Ser Arg Ala Val Ser Ile Ser Ile
204 305   310   315   320
206 Ile Glu Pro Gly Glu Glu Gly Pro Thr Ala Gly Ser Val Gly Gly Ser
207   325   330   335
209 Gly Leu Gly Thr Leu Ala Leu Ala Leu Gly Ile Leu Gly Gly Leu Gly

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212 Thr Ala Ala Leu Leu Ile Gly Val Ile Leu Trp Gln Arg Arg Gln Arg
213        355              360      .        365
215 Arg Gly Glu Glu Arg Lys Ala Pro Glu Asn Gln Glu Glu Glu Glu Glu
216    370          375              380
218 Arg Ala Glu Leu Asn Gln Ser Glu Glu Pro Glu Ala Gly Glu Ser Ser
219 385          390              395              400
221 Thr Gly Gly Pro
225 <210> SEQ ID NO: 4
226 <211> LENGTH: 1391
227 <212> TYPE: DNA
228 <213> ORGANISM: Human
230 <400> SEQUENCE: 4
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232 gtaggtgctc aaaacatcac agcccggatt ggcgagccac tggtgctgaa gtgtaagggg 120
233 gcccccaaga aaccacccca gcggctggaa tggaaactga acacaggccg gacagaagct 180
234 tggaaggtcc tgtctcccca ggggaggaggc ccctgggaca gtgtggctcg tgtccttccc 240
235 aacggctccc tcttccttcc ggctgtcggg atccaggatg aggggatttt ccggtgcagg 300
236 gcaatgaaca ggaatggaaa ggagaccaag tccaactacc gagtccgtgt ctaccagatt 360
237 cctgggaagc cagaaattgt agattctgcc tctgaactca cggctggtgt tcccaataag 420
238 gtggggacat gtgtgtcaga gggaagctac cctgcaggga ctcttagctg gcacttggat 480
239 gggaagcccc tggtgcctaa tgagaaggga gtatctgtga aggaacagac caggagacac 540
240 cctgagacag ggctcttcac actgcagtcg gagctaatgg tgaccccagc ccggggagga 600
241 gatccccgtc ccaccttctc ctgtagcttc agcccaggcc ttccccgaca ccgggccttg 660
242 cgcacagccc ccatccagcc ccgtgtctgg gagcctgtgc ctctggagga ggtccaattg 720
243 gtggtggagc cagaaggtgg agcagtagct cctggtggaa ccgtaacccct gacctgtgaa 780
244 gtccctgccc agccctctcc tcaaatccac tggatgaagg atggtgtgcc cttgcccctt 840
245 cccccagcc ctgtgctgat cctccctgag ataggcctc aggaccaggg aacctacagc 900
246 tgtgtggcca cccattccag ccacgggccc caggaaagcc gtgctgtcag catcagcatc 960
247 atcgaaccag gcgaggaggg gccaactgca ggctctgtgg gaggatcagg gctgggaact 1020
248 ctagccctgg ccctggggat cctgggaggc ctggggacag ccgccctgct cattggggtc 1080
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251 actgagggc cttgaggggc ccacagacag atcccatcca tcagctccct tttctttttc 1260
252 ccttgaactg ttctggcctc agaccaactc tctcctgtat aatctctctc ctgtataacc 1320
253 ccaccttgcc aagctttctt ctacaaccag agcccccac aatgatgatt aaacacctga 1380
254 cacatcttgc a                                                 1391
257 <210> SEQ ID NO: 5
258 <211> LENGTH: 403
259 <212> TYPE: PRT
260 <213> ORGANISM: Mouse
262 <400> SEQUENCE: 5
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266 Trp Gly Ala Val Ala Gly Gly Gln Asn Ile Thr Ala Arg Ile Gly Glu
267            20              25              30
269 Pro Leu Val Leu Ser Cys Lys Gly Ala Pro Lys Lys Pro Pro Gln Gln
270        35              40              45
272 Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu
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273         50                      55                      60
275  Ser Pro Gln Gly Gly Pro Trp Asp Ser Val Ala Gln Ile Leu Pro Asn
276  65                      70                      75                      80
278  Gly Ser Leu Leu Leu Pro Ala Thr Gly Ile Val Asp Glu Gly Thr Phe
279                      85                      90                      95
281  Arg Cys Arg Ala Thr Asn Arg Arg Gly Lys Glu Val Lys Ser Asn Tyr
282                      100                     105                     110
284  Arg Val Arg Val Tyr Gln Ile Pro Gly Lys Pro Glu Ile Val Asp Pro
285                      115                     120                     125
287  Ala Ser Glu Leu Thr Ala Ser Val Pro Asn Lys Val Gly Thr Cys Val
288          130                     135                     140
290  Ser Glu Gly Ser Tyr Pro Ala Gly Thr Leu Ser Trp His Leu Asp Gly
291  145                     150                     155                     160
293  Lys Leu Leu Ile Pro Asp Gly Lys Glu Thr Leu Val Lys Glu Glu Thr
294                      165                     170                     175
296  Arg Arg His Pro Glu Thr Gly Leu Phe Thr Leu Arg Ser Glu Leu Thr
297                      180                     185                     190
299  Val Ile Pro Thr Gln Gly Gly Thr Thr His Pro Thr Phe Ser Cys Ser
300          195                     200                     205
302  Phe Ser Leu Gly Leu Pro Arg Arg Pro Leu Asn Thr Ala Pro Ile
303          210                     215                     220
305  Gln Leu Arg Val Arg Glu Pro Gly Pro Pro Glu Gly Ile Gln Leu Leu
306  225                     230                     235                     240
308  Val Glu Pro Glu Gly Gly Ile Val Ala Pro Gly Gly Thr Val Thr Leu
309                      245                     250                     255
311  Thr Cys Ala Ile Ser Ala Gln Pro Pro Pro Gln Val His Trp Ile Lys
312          260                     265                     270
314  Asp Gly Ala Pro Leu Pro Leu Ala Pro Ser Pro Val Leu Leu Leu Pro
315          275                     280                     285
317  Glu Val Gly His Ala Asp Glu Gly Thr Tyr Ser Cys Val Ala Thr His
318          290                     295                     300
320  Pro Ser His Gly Pro Gln Glu Ser Pro Pro Val Ser Ile Arg Val Thr
321  305                     310                     315                     320
323  Glu Thr Gly Asp Glu Gly Pro Ala Glu Gly Ser Val Gly Glu Ser Gly
324                      325                     330                     335
326  Leu Gly Thr Leu Ala Leu Ala Leu Gly Ile Leu Gly Gly Leu Gly Val
327          340                     345                     350
329  Val Ala Leu Leu Val Gly Ala Ile Leu Trp Arg Lys Arg Gln Pro Arg
330          355                     360                     365
332  Arg Glu Glu Arg Lys Ala Pro Glu Ser Gln Glu Asp Glu Glu Glu Arg
333          370                     375                     380
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343  <211> LENGTH: 1347
344  <212> TYPE: DNA
345  <213> ORGANISM: Mouse
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VERIFICATION SUMMARY   DATE: 08/24/2000
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